REMARKS

Claims 1-20 were pending in the application and Claims 8, 10 and 16-20 were withdrawn. Thus, Claims 1-7, 9 and 11-15 are currently pending.

Claims 1, 2, 3, 6 and 7, and Claims 9 and 11-15 dependent thereon, were rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

It is stated on page 2 of the Office Action that Claim 1 is indefinite in the recitation of "or part" with regard to the nucleic acid sequence, since a part can be as little as one nucleotide. Applicants have amended Claim 1 to replace "part" with "a functional subsequence". A functional subsequence will not be as little as one nucleotide. Support for this amendment can be found at least on page 11 in the definition of the term "essentially similar" and on page 9, line 26. Claim 1 was also amended by adding the term "plant" before lysine ketoglutarate/saccharopine dehydrogenase. Support for this amendment can be found in the specification on page 31. Thus, no new matter has been added.

It is stated on page 2 of the Office Action that Claims 2, 3 and 7 are indefinite in the recitation of "essentially similar" given that it is unclear what the metes and bounds of this term would be regarding the claimed sequences. Claim 2 has been cancelled in view of Claim 5 and Claim 3 has been cancelled in view of Claim 4. Applicants have amended Claim 7 to recite a subsequence of the nucleic acid sequence set forth in SEQ ID NO:120. Thus, no new matter has been added.

It is stated on page 2 of the Office Action that Claim 6 is indefinite in the recitation of "subfragment thereof" with regard to the LKR gene, since a subfragment can be as little as one nucleotide. Claim 6 has been amended to replace the term "subfragment" with "functional subsequence". Once again, a functional subsequence will not be as little as one nucleotide and the Examiner's attention is kindly invited to page 9, line 26 of the specification which discusses the terms subfragment and subsequence. In addition, the claim has been reworded to clarify that seeds obtained from a plant transformed with the chimeric gene have reduced reductase activity when compared to seeds obtained from an untransformed plant. Accordingly, no new matter has been added.

In view of the amendments to Claims 1, 6 and 7, withdrawal of the rejections of these claims pursuant to 35 U.S.C. 112, first paragraph, is respectfully requested.

Claims 6, 11 and 14 were amended to recite seeds having an increased lysine content. Support for this can be found on page 31, last three lines, and in Example 23, specifically, Table 17. Thus, no new matter has been added.

In addition, claims 21-26 have been added which address blocking expressin of the LKR/SDH gene in transformed plants using antisense or cosuppression. This is discussed in the specification on page 34, last two lines through line 3 on page 36 and in the Examples. Thus, no new matter has been added.

Claims 1-3, 6, 7, 9 and 11-15 were rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

It is stated on page 4 of the Office Action that the specification fails to describe structural features that are essential for LKR activity. The Examiner's attention is kindly invited to pages 31-35 and Example 20 on pages 92-98 of the specification which describe the isolation of an *Arabidopsis* and corn lysine ketoglutarate reductase/saccharopine dehydrogenase (LKR/SDH) gene.

The discussion on pages 31-35 indicates that:

> The deduced amino acid sequence of *Arabidopsis* LKR/SDH protein is shown in SEQ ID NO:112. The amino acid sequence shows that in plants LKR and SDH enzyme activities are carried on a single bi-functional protein, and that the protein lacks an N-terminal targeting sequence indicating that the lysine degradative pathway is located in the plant cell cytosol. The amino acid sequence of *Arabidopsis* LKR/SDH protein was compared to that of other LKR and SDH proteins thus revealing regions of conserved amino acid sequence. Degenerate oligonucleotides can be designed based upon this information and used to amplify genomic or cDNA fragments via PCR from other organisms, preferably plants. As an example of this, SEQ ID NO:113 and SEQ ID NO:114 were designed and used to amplify soybean and corn LKR/SDH cDNA fragments. The sequence of a partial soybean LKR/SDH cDNA is shown in SEQ ID NO:115, and the sequence of a partial corn cDNA is shown in SEQ ID NO:116. These DNA fragments can be used to isolate larger genomic DNA fragments, which include the entire coding region, as well as 5' and 3' flanking regions, via hybridization to corn or soybean genomic DNA or cDNA libraries, as was done for *Arabidopsis*. More complete sequence information from the coding regions for soybean and corn LKR/SDH was obtained using the sequences in SEQ ID NOS:115 and 116 as starting materials in protocols such as 5' RACE and hybridization to cDNA libraries. A near full-length cDNA for soybean LKR/SDH is shown in SEQ ID NO:119, and a near full-length cDNA for corn LKR/SDH is shown in SEQ ID NO:120. A truncated version of the LKR/SDH cDNA from corn is set forth in SEQ ID NO:123.
>
> The deduced partial amino acid sequences of soybean LRK/SDH protein is shown in SEQ ID NOS:117 and 121 and the deduced partial amino acid sequences of corn LKR/SDH protein is shown in SEQ ID NO:118, 122 and 124. These amino acid sequences can be compared to other LKR/SDH protein sequences, e.g., the *Arabidopsis* LKR/SDH protein sequence, thus revealing regions of conserved amino acid sequence. With this information oligonucleotide primers can be designed and synthesized to permit isolation of LKR/SDH genomic or cDNA fragments from any plant source.

In addition, submitted herewith is a copy of Epelbaum et al., *Plant Mol. Biol.* 35:735-748 (1997) entitled "Lysine-ketoglutarate reductase and saccharopine

dehydrogenase from *Arabidopsis thaliana*: nucleotide sequence and characterization." The authors are also the co-inventors of the above-identified application. It is noted that Applicants were the first to report of the molecular cloning of a plant LKR/SDH genomic and cDNA sequence. The Epelbaum paper describes how LKR and SDH specific activity was determined using previously described assays with some minor modifications. A diagram of the *Arabidopsis* LKR-SDH gene structure is shown in Figure 3 of the Epelbaum paper.

It is stated on page 96 of the specification that:

> The complete genomic sequence of the *Arabidopsis* LKR/SDH gene is shown in SEQ ID NO:110. The sequence includes approximately 2 kb of 5' noncoding sequence and 500 bp of 3' noncoding sequence and 23 introns. Overlapping fragments of the corresponding cDNA were isolated from total *Arabidopsis* RNA by RT-PCR. **Sequence analysis of the LKR-SDH cDNA revealed an ORF of 3.16 kb, which predicts a protein of 117 kd, and confirms that the LKR and SDH enzymes reside on one polypeptide.** The complete protein coding sequence of *Arabidopsis* LKR/SDH gene, derived from the cDNA, is shown in SEQ ID NO:111. The deduced amino acid sequence of *Arabidopsis* LKR/SDH protein is shown in SEQ ID NO:112. The protein lacks an N-terminal targeting sequence implying that the lysine degradative pathway is located in the plant cell cytosol.
>
> Degenerate oligonucleotides, SEQ ID NO:113 and SEQ ID NO:114, were designed based upon comparison of the *Arabidopsis* LKR/SDH amino acid sequence with that of other LKR proteins. These were used to amplify soybean and corn LKR/SDH cDNA fragments using PCR from mRNA, or cDNA synthesized from mRNA, isolated from developing soybean or corn seeds. The soybean and corn PCR-generated cDNA fragments were cloned and sequenced. The sequence of the soybean LKR/SDH cDNA fragment is shown in SEQ ID NO:115, and the sequence of the corn cDNA fragment is shown in SEQ ID NO:116. The deduced partial amino acid sequence of soybean LKR/SDH protein is shown in SEQ ID NO:117 and the deduced partial amino acid sequence of corn LKR/SDH protein is shown in SEQ ID NO:118. The partial cDNAs encoding corn and soybean LKR/SDH obtained by PCR, above, were used in protocols that extended the sequence information for these functions. These protocols, which included RACE and direct DNA:DNA hybridization to cDNA libraries for the identification of overlapping clones, are well known to persons skilled in the art. From these efforts, more complete sequences for the corn and soybean cDNAs for LKR/SDH were obtained. **SEQ ID NOS:119 and 120 list, respectively, near full-length sequences for the LKR/SDH coding regions from soybean and corn. The deduced protein sequences encoded by these soybean and corn cDNAs are shown in SEQ ID NOS:121 and 122, respectively.** (Emphasis added.)

Other references that demonstrate that the nucleotide sequences described in the invention encode plant LKR and SDH proteins are Tang et al., *Plant Cell* 9:1305-1316 (1997) entitled "Regulation of lysine catabolism through lysine-ketoglutarate reductase and saccharopine dehydrogenase in *Arabidopsis*" (discussed below) and Kemper et al., *Eur. J. Biochem.* 253:720-729 (1998) entitled "Structure and regulation of the bifunctional enzyme lysine-oxoglutarate reductase-saccharopine dehydrogenase in maize" (both articles are submitted herewith). Kemper et al. do not disclose the nucleotide or amino acid sequence of their bifunctional corn LKR/SDH, but they do use limited proteolysis to assess the structure/function of this enzyme.

It is respectfully submitted that the foreoing clearly demonstrates a correlation between structure and function. Thus, it is respectfully submitted in view of the above discussion and information and given the teachings in the art regarding the correlation between structure and function one skilled in the art would conclude that the inventors were in possession of the claimed invention at the time the application was filed. Accordingly, withdrawal of the rejections pursuant to 35 U.S.C. 112, first paragraph, is respectfully requested.

Claims 1-7, 9 and 11-15 were rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

It is stated on page 4 of the Office Action that "the specification does not demonstrate that any of the claimed sequences encode a protein having LKR activity."

Submitted herewith is a copy of Tang et al., The Plant Cell, Vol. 9, 1305-1316 (August 1997) which is entitled "Regulation of Lysine Catabolism through Lysine-Ketoglutarate Reductase and Saccharopine Dehydrogenase in Arabidopsis". This paper reports the cloning of an Arabidopsis cDNA encoding a bifunctional polypeptide that contains both of these enzyme activities linked to each other.

The Arabidopsis sequence disclosed in this paper is identical to SEQ ID NO:111 that has been disclosed in Applicant's earlier filed cases of which priority is claimed.

It is stated on page 1308, right-hand column, of Tang et al. that:

> To determine further whether the N-terminal part of cAt-LKR/SDH encodes an LKR enzyme, the entire coding sequence of this cDNA was subcloned into the bacterial expression vector pET-15b and used to transform *E. coli* cell.s Bacterial cells harboring this plasmid had SDH but no LKR activity (data not shown). Because bacterial cells did not produce an active LKR we attempted to express the *Arabidopsis* LKR protein in yeast cells. Yeast has a monofunctional LKR enzyme, so we subcloned the N terminus of the presumed LKR domain of Cat-LKR/SDH into the yeast expression vector pVT-102u and transformed this plasmid into the yeast Lys 1 mutant. **As shown in Figure 9, yeast cells harboring this plasmid have significantly higher LKR activity than do control cells transformed with the same plasmid without the LKR insert, thereby confirming our supposition that cAT-LKR/SDH indeed encodes a bifunctional LKR/SDH enzyme.** (Emphasis added).

It is noted that on page 35 of the specification, last full paragraph, it is stated that "High level expression of *Arabidopsis* SDH was achieved in *E. coli* and the SDH protein has been purified from the bacterial extracts, and used to raise rabbit antibodies to the protein." Given, that the Arabidopsis sequence (SEQ ID NO:111) disclosed in the instant application is identical to that described by Tang et al., it

would be expected that this sequence would produce LKR activity if expressed in yeast as described by Tang et al.

Structural and Functional properties of the bifunctional LKR/SDH enzyme are discussed in the Tang et al. paper on starting on page 1312, left hand column.

Analysis of LKR and SDH activities is described on page 1315, left hand column, and it should be clear to those skilled in the art that such analysis would not require any undue experimentation.

Submitted herewith is a copy of a Declaration of Dr. Carl Falco, one of the co-inventors of the subject case, (the original version can be found in the file of Application No. 08/823,771 (Attorney Docket No. BB-1037-D)). Please note that priority of the '771 application was claimed. Dr. Falco's Declaration dated August 24, 2000, shows that with the *Arabidopsis* LKR/SDH fragments in hand, it was possible to isolate LKR/SDH fragments from any other plant desired, and use them to block expression utilizing antisense inhibition and/or cosuppression. Dr. Falco's Declaration demonstrated that blocking the first step in lysine catabolism, i.e., "knocking out" LKR/SDH, leads to increased accumulation of lysine in seeds. It is stated specifically in paragraph 9 of Dr. Falco's August 24, 2000 declaration that :

> 9. The corn LKR/SDH cDNA sequence was used to identify transposon mutations in the endogenous corn LKR/SDH gene via PCR screening of a library of corn lines containing Robertson's Mutator transposon insertions. The precise location of Mutator insertions into the LKR/SDH gene was determined by sequencing of genomic DNA from individual mutants. An insertion mutation located in an exon in the LKR domain of the gene was chosen for further study. Southern blot analysis of corn genomic DNA indicated that corn contains only one LKR/SDH gene. Since an insertion mutation is expected to block function of the gene, it was anticipated that such a mutation would be recessive. One fourth of the progeny seed from a selfed corn ear with such a mutation segregating would be expected to be homozygous for the mutation. It was observed that approximately one fourth of such seed exhibited a higher level of free lysine than normal (5 to 15 fold higher) without the increase in the lysine catabolite saccharopine that is seen when free lysine is increased via expression of lysine insensitive DHDPS. It was concluded that knocking out LKR/SDH, by itself, was able to increase seed lysine content in corn seeds.
>
> The LKR/SDH Mutator insertion line was crossed by a transgenic line that accumulates excess free lysine due to expression of lysine insensitive DHDPS and AK. In this cross two genetic loci that affect lysine accumulation, one of which is recessive (the LKR/SDH Mutator insertion) and one of which is semi-dominant (the lysine insensitive DHDPS and AK trangene locus), are segregating. Single seeds were analyzed for lysine and saccharopine content. The most striking observation from this experiment is that the highest lysine containing seeds have low levels of saccharopine (see figure). The low saccharopine level indicates that these seeds are homozygous for the LKR/SDH Mutator insertion, while the high lysine level indicates that they carry the lysine insensitive DHDPS and AK trangene locus. The level of lysine accumulation is considerably higher (2-3 fold) than the level provided by the DHDPS and AK trangene locus alone. Thus, this experiment demonstrates that an increase in the accumulation of lysine, accompanied by a reduction in accumulation of lysine catabolites can be accomplished by combination of lysine overproduction brought about by expression of lysine insensitive DHDPS + AK and reduction of lysine catabolism by blocking expression of LKR/SDH, as we taught in the patent application. These results show that the concern stated in the Office Action on page 5 that

"modifying metabolic pathways ... is highly unpredictable and often the desirable results are impossible to achieve" is unfounded in this particular case.

As indicated above, LKR/SDH expression has been blocked in corn via cosuppression. To accomplish this a chimeric gene designed for cosuppression of LKR was constructed by linking a 1268 bp LKR/SDH gene fragment, which included the LKR coding domain, to the corn endosperm 27 kD zein promoter and 10 kD zein 3' untranslated region. This chimeric gene was introduced into corn by particle-gun mediated transformation. Over 100 transformed lines were obtained. Of 72 transformation events that were regenerated into plants and produced seed, 13 had seeds with a greater than four fold increase in free lysine. This is a typical frequency for cosuppression events. Since the transformed plants were out-crossed, the transgenic locus must be dominant or there would not have been any observable phenotype. This is expected from a cosuppression transgene, and is an advantage over knock-out mutations like the LKR/SDH Mutator insertion described above.

Some of the LKR cosuppression transformants have been carried forward for further testing. An event that has continued to show the increased free lysine phenotype for several generations and behaves genetically as a single locus transgene insertion has been selected for crossing to the transgenic line that accumulates excess free lysine due to expression of lysine insensitive DHDPS and AK. Results from that experiment are not yet available, but the expectation is that seeds carrying both transgene loci will have higher lysine levels than either parent, as was observed in the LKR Mutator insertion cross described above. In addition, co-transformation experiments in which the chimeric gene designed for cosuppression of LKR described above has been combined with a chimeric gene for expression of lysine insensitive DHDPS and introduced into corn by particle-gun mediated transformation are in progress. This is expected to yield transformants that produce seeds with the high lysine level observed in the LKR Mutator insertion cross by lysine insensitive DHDPS and AK, but with both chimeric genes at a single genetic locus, which is highly desirable for corn breeding.

Also submitted herewith is a copy of a second Declaration of Dr. Carl Falco, (the original version can be found in the file of Application No. 08/823,771 (Attorney Docket No. BB-1037-D)). Once again, please note that priority of the '771 application was claimed. Dr. Falco's Declaration dated February 16, 2001, sets forth data showing seeds with increased lysine that were obtained from plants co-transformed with DHDPS and LKR.

The experiments discussed in Dr. Falco's Declaration dated February 16, 2001 along with the information submitted herewith and the detailed description of the invention provided in the instant application demonstrate that seeds having an increased lysine content can be made when a lysine insensitive DHDPS gene (with or without a lysine insensitive AK gene) is combined with a co-suppressing LKR gene.

It is stated on page 4 of the Office Action that "It is well established that sequence similarity is not sufficient to determine functionality of a cDNA coding sequence."

Applicants respectfully submit that in view of Tang et al. it is clear that there is a correlation between sequence similarity and functionality insofar as LKR/SDH activity is concerned.

Thus, it is respectfully submitted in view of the above discussion and references, that no undue experimentation would be needed to practice the claimed invention. Accordingly, withdrawal of the rejections pursuant to 35 U.S.C. 112, first paragraph, is requested.

It is respectfully submitted that the application is in form for allowance which allowance is respectfully requested.

A petition for a two (2) month extension of time, a version with markings to show changes made and copies of the above-identified documents accompany this response.

The Commissioner is authorized to charge Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company) for any fees associated with the filing of this response.

Respectfully submitted,

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VERSION WITH MARKING TO SHOW CHANGES MADE

In showing the changes, deleted material is shown in bolded brackets and stricken through, and inserted material is shown underlined.

IN THE CLAIMS:

1. (once amended) An isolated nucleic acid fragment comprising a nucleic acid sequence encoding all or [part] a functional subsequence of a plant [lysine ketoglutarate reductase] lysine ketoglutarate reductase/saccharopine dehydrogenase.

4. (once amended) The nucleic acid fragment of Claim 1 comprising a nucleic acid sequence of [SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:119,] SEQ ID NO:120[, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129 or SEQ ID NO:131].

5. The nucleic acid fragment of Claim 1 wherein the nucleic acid sequence encodes a polypeptide as set forth in [SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:112, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:121,] SEQ ID NO:122[, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130 or SEQ ID NO:132].

6. (once amended) A chimeric gene comprising the isolated nucleic acid fragment of Claim 1 encoding lysine ketoglutarate reductase or a [subfragment] functional subsequence thereof, operably linked to suitable seed-specific regulatory sequences wherein a plant transformed with said chimeric gene has seeds with [reduced slysine ketoglutarate reductase activity] increased lysine content compared to [in] seeds obtained from untransformed [of] plants [transformed with the chimeric gene].

7. (once amended) The chimeric gene according to Claim 6 wherein the isolated nucleic acid fragment comprises a nucleic acid sequence or functional subsequence thereof [essentially similar to that of] as set forth in [SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:119,] SEQ ID NO:120[, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129 or SEQ ID NO:131].

11. (once amended) A plant seed transformed with the chimeric gene of Claim 6 or 7 wherein said transformed plant seed has [reduced lysine ketoglutarate reductase activity] an increased lysine content compared to seed obtained from an untransformed plant.

14. (once amended) A method for [reducing lysine ketoglutarate reductase activity] increasing lysine content in a plant seed which comprises:

(a) transforming plant cells with the chimeric gene of claim 6 or 7;

(b) regenerating fertile mature plants from the transformed plant cells obtained from step (a) under conditions suitable to obtain seeds;

(c) screening progeny seed of step (b) for [reduced lysine ketoglutarate reductase activity] increased lysine content; and

(d) selecting those lines whose seeds [contain reduced lysine ketoglutarate reductase activity] have increased lysine content.

Kindly add the following new claims:

21. (new) An isolated nucleic acid fragment comprising a nucleic acid sequence which is useful in antisense inhibition or sense suppression of endogenous lysine ketoglutarate reductase activity in a transformed plant wherein said isolated nucleic acid fragment comprises all or part of the nucleic acid sequence of SEQ ID NO:120.

22. (new) A chimeric gene capable of causing an increased level of lysine in seeds obtained from a transformed plant, the chimeric gene comprising a nucleic acid fragment of Claim 21, said fragment being operably linked to at least one regulatory sequence.

23. (new) Plants comprising the chimeric gene of claim 22 in their genome.

24. (new) Seeds obtained from the plants of claim 23.

25. (new) The plants of claim 23 wherein said plants are selected from the group of plants consisting of *Arabidopsis*, corn, soybean, rapeseed, wheat and rice.

26. (new) A method for increasing lysine content in a plant seed which comprises:

(a) transforming plant cells with the chimeric gene of claim 21;

(b) regenerating fertile mature plants from the transformed plant cells obtained from step (a) under conditions suitable to obtain seeds;

(c) screening progeny seed of step (b) for increased lysine content; and

(d) selecting those lines whose seeds have increased lysine content.

27. (new) The method of claim 27 wherein said plant cell is selected from the group of plants consisting of *Arabidopsis*, corn, soybean, rapeseed, wheat and rice.

28. (new) Plant seed obtained by the method of claim 26 or 27.

IN THE SPECIFICATION:

Pleas delete th sequ nc listing appearing on pag 8 in its ntirety and on page 9 through SEQ ID NO:132 with the following:

SEQ ID NOS:102 and 103 are partial cDNAs for plant lysine ketoglutarate reductase/saccharopine dehydrogenase from *Arabidopsis thaliana*.

SEQ ID NOS:104 and 105 are polypeptides encoded by SEQ ID NOS:102 and 103, respectively that are homologous to fungal saccharopine dehydrogenase (glutamate-forming) [encoded by SEQ ID NOS:102 and 103, respectively].

SEQ ID NOS:106 and 107 were used in Example 25 as PCR primers to add Nco I and Kpn I sites at the 5' and 3' ends of the corn DHDPS gene.

SEQ ID NOS:108 and 109 were used for PCR amplification of a 2.24 kb DNA fragment from genomic *Arabidopsis* DNA.

SEQ ID NO:110 shows the sequence of the *Arabidopsis* [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase genomic DNA fragment.

SEQ ID NO:111 shows the [sequence of the Arabidopsis LKR/SDH cDNA] sequence of a full length cDNA[s] for plant lysine ketoglutarate reductase/saccharopine dehydrogenase from *Arabidopsis thaliana*.

SEQ ID NO:112 shows the deduced amino acid sequence of *Arabidopsis* [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein.

SEQ ID NOS:113 and 114 were used for PCR amplification of soybean and corn [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase cDNA fragment.

SEQ ID NO:115 shows the sequence of a soybean [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase cDNA fragment.

SEQ ID NO:116 shows the sequence of a corn [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase cDNA fragment.

SEQ ID NO:117 shows the [deduced] partial amino acid sequence of soybean [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein deduced from SEQ ID NO:115.

SEQ ID NO:118 shows the [deduced] partial amino acid sequence of corn [LRK/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein deduced from SEQ ID NO:116.

SEQ ID NO:119 shows the sequence of a 2582 nucleotide partial cDNA from soybean for a lysine ketoglutarate reductase/saccharopine dehydrogenase protein.

SEQ ID NO:120 shows the sequence of a 3265 nucleotide partial cDNA from corn for a lysine ketoglutarate reductase/saccharopine dehydrogenase protein.

.SEQ ID NO:121 shows the deduced partial amino acid sequence of soybean [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein encoded by nucleotides 3 through 2357 of SEQ ID NO:119.

SEQ ID NO:122 shows the deduced partial amino acid sequence of [soybean] corn [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein encoded by nucleotides 3 through 3071 of SEQ ID NO:120.

SEQ ID NO:123 is a nucleotide sequence corresponding to nucleotides 1 through 1908 of SED ID NO:120.

SEQ ID NO:124 is the deduced amino acid sequence from SEQ ID NO:123.

SEQ ID NO:125 shows the sequence of a 720 nucleotide [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase cDNA from rice.

SEQ ID NO:126 shows the deduced partial amino acid sequence of rice [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein encoded by nucleotides 2 through 720 of SEQ ID NO:125.

SEQ ID NO:127 shows the sequence of a 308 nucleotide [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase cDNA from rice.

SEQ ID NO:128 shows the deduced partial amino acid sequence of rice [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein encoded by nucleotides 1 through 129 of SEQ ID NO:127.

SEQ ID NO:129 shows the sequence of a 429 nucleotide cDNA from wheat.

SEQ ID NO:130 shows the deduced partial amino acid sequence of wheat [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein encoded by nucleotides 1 through 252 of SEQ ID NO:129.

SEQ ID NO:131 shows the SDH coding region of the *Arabidopsis* cDNA clone.

SEQ ID NO:132 shows the amino acid sequence of the [SDH] saccharopine dehydrogenase[.] domain of the *Arabidopsis* [LKR/SDH] lysine ketoglutarate reductase/saccharopine dehydrogenase protein.